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DNA ENCODING HUMAN SERINE PROTEASE D-G

5 BACKGROUND OF THE INVENTION

Members of the trypsin/chymotrypsin-like (S1) serine protease family play pivotal roles in a multitude of diverse physiological processes, including digestive processes and regulatory amplification cascades through the proteolytic activation of inactive zymogen precursors. In many instances protease substrates within these cascades are themselves the inactive form, or zymogen, of a "downstream" serine protease. Well-known examples of serine protease-mediated regulation include blood coagulation, (Davie, et al. (1991). *Biochemistry* 30:10363-70), kinin formation (Proud and Kaplan (1988). *Ann Rev Immunol* 6: 49-83) and the complement system (Reid and Porter (1981). *Ann Rev Biochemistry* 50:433-464). Although these proteolytic pathways have been known for sometime, it is likely that the discovery of novel serine protease genes and their products will enhance our understanding of regulation within these existing cascades, and lead to the elucidation of entirely novel protease networks.

Proteases are used in non-natural environments for various commercial purposes including laundry detergents, food processing, fabric processing and skin care products. In laundry detergents, the protease is employed to break down organic, poorly soluble compounds to more soluble forms that can be more easily dissolved in detergent and water. In this capacity the protease acts as a "stain remover." Examples of food processing include tenderizing meats and producing cheese.

Proteases are used in fabric processing, for example, to treat wool in order prevent fabric shrinkage. Proteases may be included in skin care products to remove scales on the skin surface that build up due to an imbalance in the rate of desquamation. Common proteases used in some of these applications are derived from prokaryotic or eukaryotic cells that are easily grown for industrial manufacture of their enzymes, for example a common species used is *Bacillis* as described in United States patent

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5,217,878. Alternatively, United States Patent 5,278,062 describes serine proteases isolated from a fungus, *Tritirachium album*, for use in laundry detergent compositions. Unfortunately use of some proteases is limited by their potential to cause allergic reactions in sensitive individuals or by reduced efficiency when used in a non-natural environment. It is anticipated that protease proteins derived from non-human sources would be more likely to induce an immune response in a sensitive individual. Because of these limitations, there is a need for alternative proteases that are less immunogenic to sensitive individuals and/or provides efficient proteolytic activity in a non-natural environment. The advent of recombinant technology allows expression of any species' proteins in a host suitable for industrial manufacture.

Herein we describe a novel serine protease isolated from small intestine termed D-G. The deduced amino acid sequence encodes a polypeptide of 435 amino acids. Interestingly, the sequence contains a hydrophobic stretch of amino acids which is a putative transmembrane near the NH₂-terminus. Thus, this serine protease is thought to be synthesized as a type II integral membrane protein. Alignment with other well characterized serine proteases clearly indicates that it is a member of the S1 serine protease family with the catalytic triad residing within the C-terminal half of the molecule. The protease D-G deduced amino acid sequence is most similar to the cloned serine proteases TMPRSS2 (Paoloni-Giacobino et al. (1997). *Genomics* 44:309-320) and hepsin (Leytus et al. (1988). *Biochemistry* 27:1067-74), which are also type II integral membrane proteases. We have found that the protease D-G mRNA is widely expressed in several tissues throughout the body including epidermis, fibroblasts, keratinocytes, colon, small intestine, stomach, lung, kidney, bone marrow, lymph node, thymus, ovary, prostate, uterus and spinal cord. Altered expression or regulation of this enzyme may be responsible for any one of a number of pathological conditions in these tissues. Furthermore, an up-regulation whereby under normal physiological conditions protease D-G mRNA is not expressed, and therefore undetected, but in the pathogenic condition it is markedly elevated could potentially result in initiating or exacerbation of certain diseased states. We

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expressed a soluble form of this novel human protease by inserting the portion of the protease D-G cDNA, encoding the catalytic domain, in a zymogen activation construct designed to permit the generic activation of heterologous serine protease catalytic domains. The result is an active preparation of protease D-G that has an activity against a subset of amidolytic substrates. Isolation of purified, enzymatically active protease D-G allows the protein to be used directly, for example to discover chemical modulators of the enzyme or as an additive in commercial products. Because protease D-G is derived from a human host, it is less likely to induce an allergic reaction in sensitive individuals, and therefore protease D-G may also be useful for formulation of compositions for laundry detergents and skin care products.

SUMMARY OF THE INVENTION

A DNA molecule encoding protease D-G has been cloned and characterized and it represents a novel serine protease. Using a recombinant expression system functional DNA molecules encoding the protease have been isolated. The biological and structural properties of these proteins are disclosed, as is the amino acid and nucleotide sequence. The recombinant DNA molecules, and portions thereof, are useful for isolating homologues of the DNA molecules, identifying and isolating genomic equivalents of the DNA molecules, and identifying, detecting or isolating mutant forms of the DNA molecules. The recombinant protein is useful to identify modulators of functional protease D-G. Modulators identified in the assays disclosed herein may be useful as therapeutic agents for cancer, skin disorders, neuropathic pain, inflammatory, or coagulation diathesis/thrombosis.

BRIEF DESCRIPTION OF THE DRAWING

Figure 1 A - The nucleotide (SEQ.ID.NO.:1) of the novel protease D-G cDNA is shown.

Figure 1 B - The amino acid sequence (SEQ.ID.NO.:2) of the novel protease D-G cDNA is shown.

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Figure 2 - The phylogenetic tree of the protease D-G amino acid sequence relative to other S1 serine proteases is shown.

Figure 3 - PCR-based tissue distribution indicates that the protease D-G mRNA is restricted. Autoradiograms of gels are shown with the position of the D-G specific PCR product, as detected by the hybridization of a labeled nested probe, which was resolved following electrophoresis from the free probe (F.P.). The cDNA libraries of tissues and cell lines analyzed are as indicated.

Figure 4 A & B- The nucleotide (SEQ.ID.NO.:8) and amino acid (SEQ.ID.NO.:9) sequences of the protease D-G catalytic domain in the zymogen activation construct are shown.

Figure 5 - Polyacrylamide gel and Western blot analyses of the purified recombinant protease PFEK-protease D-G-6XHIS. Shown is the polyacrylamide gel containing samples of the novel serine protease PFEK-protease D-G-6XHIS stained with Coomassie Brilliant Blue (lanes 2 and 3). The relative molecular masses are indicated by the positions of protein standards (lane 1). In the indicated lanes, the purified zymogen was either untreated (-) or digested (+) with enterokinase (EK) which was used to cleave and activate the zymogen of lane 1 into its active form of increased mobility shown in lane 2. Lanes 4 and 5 indicate the Western blot of the corresponding gel lanes 1 and 2, probed with the anti-FLAG MoAb M2. This demonstrates the quantitative cleavage of the expressed and purified zymogen to generate the processed and activated protease. Since the FLAG epitope is located just upstream of the of the EK pro sequence, cleavage with EK generates a FLAG-containing polypeptide which is

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too small to be retained in the polyacrylamide gel, and is therefore not detected in the +EK lane.

Figure 6 - Functional amidolytic activities of the recombinant protease D-G-6XHIS expressed, purified and activated from the activation construct were determined using the indicated chromogenic substrates.

DETAILED DESCRIPTION

Definitions

Definitions

The term “protein domain” as used herein refers to a region of a protein that may have a particular three-dimensional structure which may be independent from the remainder of the protein. This structure may maintain a particular activity associated with the domain’s function within the protein including enzymatic activity, creation of a recognition motif for another molecule, or provide necessary structural components for a protein to exist in a particular environment. Protein domains are usually evolutionarily conserved regions of proteins, both within a protein family and within protein superfamilies that perform similar functions. The term “protein superfamily” as used herein refers to proteins whose evolutionary relationship may not be entirely established or may be distant by accepted phylogenetic standards, but show similar three dimensional structure or display unique consensus of critical amino acids. The term “protein family” as used herein refers to proteins whose evolutionary relationship has been established by accepted phylogenic standards.

The term “fusion protein” as used herein refers to protein constructs that are the result of combining multiple protein domains or linker regions for the purpose of gaining the combined functions of the domains or linker regions. This is may be accomplished by molecular cloning of the nucleotide sequences encoding such domains to produce a new polynucleotide sequence that encodes the desired fusion protein. Alternatively, creation of a fusion protein may be accomplished by chemically joining two proteins.

30 The term “linker region” or “linker domain” or similar such descriptive terms as used herein refers to polynucleotide or polypeptide sequence that are used in the

construction of a cloning vector or fusion protein. Functions of a linker region can include introduction of cloning sites into the nucleotide sequence, introduction of a flexible component or space-creating region between two protein domains, or creation of an affinity tag for specific molecule interaction. A linker region may be introduced into a fusion protein resulting from choices made during polypeptide or nucleotide sequence construction.

The term "cloning site" or "polycloning site" as used herein refers to a region of the nucleotide sequence that has one or more available restriction endonuclease consensus cleavage sequences. These nucleotide sequences may be used for a variety of purposes, including but not limited to introduction into DNA vectors to create novel fusion proteins, or to introduce specific site-directed mutations. It is well known by those of ordinary skill in the art that cloning sites can be engineered at a desired location by silent mutations, conserved mutation, or introduction of a linker region that contains desired restriction enzyme consensus sequences. It is also well known by those of ordinary skill in the art that the precise location of a cloning site can be engineered into any location in a nucleotide sequence.

The term “tag” as used herein refers to an amino acid sequence or a nucleotide sequence that encodes an amino acid sequence, that facilitates isolation, purification or detection of a protein containing the tag. A wide variety of such tags are known to those skilled in the art, and are suitable for use in the present invention. Suitable tags include, but are not limited to, HA peptide, polyhistidine peptides, biotin / avidin, and other antibody epitope binding sites.

25 *Isolation of protease D-G nucleic acid*

25 The present invention relates to DNA encoding the human serine protease D-G which was isolated from cells of small intestine. Protease D-G, as used herein, refers to protein which can specifically function as a protease.

The complete amino acid sequence of protease D-G was not previously
30 known, nor was the complete nucleotide sequence encoding protease D-G known.
It is predicted that a wide variety of cells and cell types will contain the described

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protease D-G mRNA. Tissues capable of producing protease D-G include, but are not limited to epidermis, fibroblasts, keratinocytes, colon, small intestine, stomach, lung, kidney, bone marrow, lymph node, thymus, ovary, prostate, uterus and spinal cord as we have determined by a sensitive polymerase chain reaction

5 (PCR)-mediated mRNA detection methodology.

Other cells and cell lines may also be suitable for use to isolate protease D-G cDNA. Selection of suitable cells may be done by screening for protease D-G activity in cell extracts or in whole cell assays, described herein. Cells that possess protease D-G activity in any one of these assays may be suitable for the

10 isolation of protease D-G DNA or mRNA.

Any of a variety of procedures known in the art may be used to molecularly clone protease D-G DNA. These methods include, but are not limited to, direct functional expression of the protease D-G genes following the construction of a protease D-G-containing cDNA library in an appropriate

15 expression vector system. Another method is to screen protease D-G-containing cDNA library constructed in a bacteriophage or plasmid shuttle vector with a labelled oligonucleotide probe designed from the amino acid sequence of the protease D-G subunits. An additional method consists of screening a protease D-G-containing cDNA library constructed in a bacteriophage or plasmid shuttle

20 vector with a partial cDNA encoding the protease D-G protein. This partial cDNA is obtained by the specific PCR amplification of protease D-G DNA fragments through the design of degenerate oligonucleotide primers from the amino acid sequence of the purified protease D-G protein.

Another method is to isolate RNA from protease D-G-producing cells and

25 translate the RNA into protein via an *in vitro* or an *in vivo* translation system. The translation of the RNA into a peptide a protein will result in the production of at least a portion of the protease D-G protein which can be identified by, for example, immunological reactivity with an anti-protease D-G antibody or by biological activity of protease D-G protein. In this method, pools of RNA isolated

30 from protease D-G-producing cells can be analyzed for the presence of an RNA

that encodes at least a portion of the protease D-G protein. Further fractionation of the RNA pool can be done to purify the protease D-G RNA from non-protease D-G RNA. The peptide or protein produced by this method may be analyzed to provide amino acid sequences which in turn are used to provide primers for

10 Laboratory Press, Cold Spring Harbor, NY. 1989.

not limited to, cDNA libraries derived from other cells, from organisms other than
protease D-G, and genomic DNA libraries that include YAC (yeast artificial
chromosome) and cosmid libraries.

20 selection of cells or cell lines for use in preparing a cDNA library to isolate protease D-G cDNA may be done by first measuring cell associated protease D-G activity using the measurement of protease D-G-associated biological activity or a ligand binding assay.

25 well known in the art. Well known cDNA library construction techniques can be found for example, in Maniatis, T., Fritsch, E.F., Sambrook, J., Molecular Cloning: A Laboratory Manual, Second Edition (Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989).

It is also readily apparent to those skilled in the art that DNA encoding
30 protease D-G may also be isolated from a suitable genomic DNA library.

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Construction of genomic DNA libraries can be performed by standard techniques well known in the art. Well known genomic DNA library construction techniques can be found in Maniatis, T., Fritsch, E.F., Sambrook, J. in *Molecular Cloning: A Laboratory Manual*, Second Edition (Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989).

5 In order to clone the protease D-G gene by the above methods, the amino acid sequence of protease D-G may be necessary. To accomplish this, protease D-G protein may be purified and partial amino acid sequence determined by automated sequenators. It is not necessary to determine the entire amino acid
10 sequence, but the linear sequence of two regions of 6 to 8 amino acids from the protein is determined for the production of primers for PCR amplification of a partial protease D-G DNA fragment.

Once suitable amino acid sequences have been identified, the DNA sequences capable of encoding them are synthesized. Because the genetic code is
15 degenerate, more than one codon may be used to encode a particular amino acid, and therefore, the amino acid sequence can be encoded by any of a set of similar DNA oligonucleotides. Only one member of the set will be identical to the protease D-G sequence but will be capable of hybridizing to protease D-G DNA even in the presence of DNA oligonucleotides with mismatches. The mismatched
20 DNA oligonucleotides may still sufficiently hybridize to the protease D-G DNA to permit identification and isolation of protease D-G encoding DNA. DNA isolated by these methods can be used to screen DNA libraries from a variety of cell types, from invertebrate and vertebrate sources, and to isolate homologous genes.

25 Purified biologically active protease D-G may have several different physical forms. protease D-G may exist as a full-length nascent or unprocessed polypeptide, or as partially processed polypeptides or combinations of processed polypeptides. The full-length nascent protease D-G polypeptide may be post-translationally modified by specific proteolytic cleavage events that results in the formation of
30 fragments of the full length nascent polypeptide. A fragment, or physical association

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of fragments may have the full biological activity associated with protease D-G however, the degree of protease D-G activity may vary between individual protease D-G fragments and physically associated protease D-G polypeptide fragments.

Because the genetic code is degenerate, more than one codon may be used to encode a particular amino acid, and therefore, the amino acid sequence can be encoded by any of a set of similar DNA oligonucleotides. Only one member of the set will be identical to the protease D-G sequence but will be capable of hybridizing to protease D-G DNA even in the presence of DNA oligonucleotides with mismatches under appropriate conditions. Under alternate conditions, the mismatched DNA oligonucleotides may still hybridize to the protease D-G DNA to permit identification and isolation of protease D-G encoding DNA.

DNA encoding protease D-G from a particular organism may be used to isolate and purify homologues of protease D-G from other organisms. To accomplish this, the first protease D-G DNA may be mixed with a sample containing DNA encoding homologues of protease D-G under appropriate hybridization conditions. The hybridized DNA complex may be isolated and the DNA encoding the homologous DNA may be purified therefrom.

Functional derivatives / Variants

It is known that there is a substantial amount of redundancy in the various codons that code for specific amino acids. Therefore, this invention is also directed to those DNA sequences that contain alternative codons that code for the eventual translation of the identical amino acid. For purposes of this specification, a sequence bearing one or more replaced codons will be defined as a degenerate variation. Also included within the scope of this invention are mutations either in the DNA sequence or the translated protein, which do not substantially alter the ultimate physical properties of the expressed protein. For example, substitution of aliphatic amino acids alanine, valine, leucine and isoleucine; interchange of the hydroxyl residues serine and threonine, exchange of the acidic residues aspartic acid and glutamic acid, substitution between the amide residues asparagine and glutamine, exchange of the

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basic residues lysine and arginine and variants among the aromatic residues phenylalanine, tyrosine may not cause a change in functionality of the polypeptide. Such substitutions are well known and are described, for instance in Molecular Biology of the Gene, 4th Ed. Benjamin Cummings Pub. Co. by Watson *et al.*

5 It is known that DNA sequences coding for a peptide may be altered so as to code for a peptide having properties that are different than those of the naturally occurring peptide. Methods of altering the DNA sequences include, but are not limited to site directed mutagenesis, chimeric substitution, and gene fusions. Site-directed mutagenesis is used to change one or more DNA residues that may result in a
10 silent mutation, a conservative mutation, or a nonconservative mutation. Chimeric genes are prepared by swapping domains of similar or different genes to replace similar domains in the protease D-G gene. Similarly, fusion genes may be prepared that add domains to the protease D-G gene, such as an affinity tag to facilitate identification and isolation of the gene. Fusion genes may be prepared to replace
15 regions of the protease D-G gene, for example to create a soluble version of the protein by removing a transmembrane domain or adding a targeting sequence to redirect the normal transport of the protein, or adding new post-translational modification sequences to the protease D-G gene. Examples of altered properties include but are not limited to changes in the affinity of an enzyme for a substrate or a
20 receptor for a ligand. All such changes of the polynucleotide or polypeptide sequences are anticipated as useful variants of the present invention so long as the original function of the polynucleotide or polypeptide sequence of the present invention is maintained as described herein.

 Identity or similarity, as known in the art, are relationships between two or
25 more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, identity also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. Both identity and similarity can be readily calculated (Computational Molecular Biology, Lesk, A. M.,
30 ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and

Genome Projects, Smith, D. W., ed., Academic Press, New York, 1993; Computer Analysis of Sequence Data, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; and Sequence Analysis Primer, Gribskov, M. and Devereux, D.

Polynucleotide(s) generally refers to any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. Thus, for instance, polynucleotides as used herein refers to, among others, single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions or single-, double- and triple- stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded, or triple-stranded, or a mixture of single- and double-stranded regions. In addition, polynucleotide as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include

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all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. As used herein, the term polynucleotide includes DNAs or RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with
5 backbones modified for stability or for other reasons are "polynucleotides" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes
10 known to those of skill in the art. The term polynucleotide as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including simple and complex cells, inter alia. Polynucleotides embraces short polynucleotides often referred to as oligonucleotide(s).

15 The term polypeptides, as used herein, refers to the basic chemical structure of polypeptides that is well known and has been described in textbooks and other publications in the art. In this context, the term is used herein to refer to any peptide or protein comprising two or more amino acids joined to each other in a linear chain by peptide bonds. As used herein, the term refers to both short chains, which also
20 commonly are referred to in the art as peptides, oligopeptides and oligomers, for example, and to longer chains, which generally are referred to in the art as proteins, of which there are many types. It will be appreciated that polypeptides often contain amino acids other than the 20 amino acids commonly referred to as the 20 naturally occurring amino acids, and that many amino acids, including the terminal amino
25 acids, may be modified in a given polypeptide, either by natural processes, such as processing and other post-translational modifications, but also by chemical modification techniques which are well known to the art. Even the common modifications that occur naturally in polypeptides are too numerous to list exhaustively here, but they are well described in basic texts and in more detailed
30 monographs, as well as in a voluminous research literature, and they are well known

to those of skill in the art. Among the known modifications which may be present in polypeptides of the present are, to name an illustrative few, acetylation, acylation, ADP- ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing,

phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. Such modifications are well known to those of skill and have been described in great detail in the scientific literature. Several particularly common modifications, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, for instance, are described in most basic texts, such as, for instance *PROTEINS-- STRUCTURE AND MOLECULAR PROPERTIES*, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993). Many detailed reviews are available on this subject, such as, for example, those provided by Wold, F., *Posttranslational Protein Modifications: Perspectives and Prospects*, pgs. 1-12 in *POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS*, B. C. Johnson, Ed., Academic Press, New York (1983); Seifter et al., (1990) *Meth. Enzymol.* 182, 626-646 and Rattan et al., "Protein Synthesis: Posttranslational Modifications and Aging", (1992) *Ann. N.Y. Acad. Sci.* 663, 48-62. It will be appreciated, as is well known and as noted above, that polypeptides are not always entirely linear. For instance, polypeptides may be generally as a result of posttranslational events, including natural processing event and events brought about by human manipulation which do not occur naturally. Circular, branched and branched circular polypeptides may be synthesized by non-translation natural process and by entirely synthetic methods, as well. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the

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amino or carboxyl termini. In fact, blockage of the amino or carboxyl group in a polypeptide, or both, by a covalent modification, is common in naturally occurring and synthetic polypeptides and such modifications may be present in polypeptides of the present invention, as well. For instance, the amino terminal residue of

5 polypeptides made in *E. coli* or other cells, prior to proteolytic processing, almost invariably will be N-formylmethionine. During post-translational modification of the peptide, a methionine residue at the NH₂-terminus may be deleted. Accordingly, this invention contemplates the use of both the methionine-containing and the methionine-less amino terminal variants of the protein of the invention. The modifications that

10 occur in a polypeptide often will be a function of how it is made. For polypeptides made by expressing a cloned gene in a host, for instance, the nature and extent of the modifications in large part will be determined by the host cell posttranslational modification capacity and the modification signals present in the polypeptide amino acid sequence. For instance, as is well known, glycosylation often does not occur in

15 bacterial hosts such as, for example, *E. coli*. Accordingly, when glycosylation is desired, a polypeptide should be expressed in a glycosylating host, generally a eukaryotic cell. Insect cell often carry out the same posttranslational glycosylations as mammalian cells and, for this reason, insect cell expression systems have been developed to express efficiently mammalian proteins having native patterns of

20 glycosylation, inter alia. Similar considerations apply to other modifications. It will be appreciated that the same type of modification may be present in the same or varying degree at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. In general, as used herein, the term polypeptide encompasses all such modifications, particularly those that are present in polypeptides

25 synthesized recombinantly by expressing a polynucleotide in a host cell.

Variant(s) of polynucleotides or polypeptides, as the term is used herein, are polynucleotides or polypeptides that differ from a reference polynucleotide or polypeptide, respectively. A variant of the polynucleotide may be a naturally occurring variant such as a naturally occurring allelic variant, or it may be a variant

30 that is not known to occur naturally. (1) A polynucleotide that differs in nucleotide

sequence from another, reference polynucleotide. Generally, differences are limited so that the nucleotide sequences of the reference and the variant are closely similar overall and, in many regions, identical. As noted below, changes in the nucleotide sequence of the variant may be silent. That is, they may not alter the amino acids

polynucleotide. Such nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the

sequence by one or more substitutions, additions, deletions, fusions and truncations, which may be present in any combination. As used herein, a "functional derivative" of protease D-G is a compound that possesses a biological activity (either functional or structural) that is substantially similar to the biological activity of protease D-G.

25 example an affinity tag such as biotin, a fluorescent dye, or to conjugate the polypeptide to a solid phase surface (for example to create an affinity resin). The term "fragment" is meant to refer to any polypeptide subset of protease D-G. A molecule is "substantially similar" to protease D-G if both molecules have substantially similar structures or if both molecules possess similar biological activity.

30 Therefore, if the two molecules possess substantially similar activity, they are

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considered to be variants even if the structure of one of the molecules is not found in the other or even if the two amino acid sequences are not identical. The term "analog" refers to a molecule substantially similar in function to either the entire protease D-G molecule or to a fragment thereof. Particularly preferred in this regard are polynucleotides encoding variants, analogs, derivatives and fragments of SEQ ID NO.:1, and variants, analogs and derivatives of the fragments, which have the amino acid sequence of the polypeptide of SEQ ID NO.:2 in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the gene of SEQ ID NO.:1. Also especially preferred in this regard are conservative substitutions. Most highly preferred are polynucleotides encoding polypeptides having the amino acid sequence of SEQ ID NO.:2, without substitutions.

Further preferred embodiments of the invention are polynucleotides that are at least 70% identical over their entire length to a polynucleotide encoding the polypeptide having the amino acid sequence set out in SEQ ID NO.:2, and polynucleotides which are complementary to such polynucleotides. Alternatively, highly preferred are polynucleotides that comprise a region that is at least 80% identical, more highly preferred are polynucleotides that comprise a region that is at least 90% identical, and among these preferred polynucleotides, those with at least 95% are especially preferred. Furthermore, those with at least 97% identity are highly preferred among those with at least 95%, and among these those with at least 98% and at least 99% are particularly highly preferred, with at least 99% being the most preferred. The polynucleotides which hybridize to the polynucleotides described herein in a preferred embodiment encode polypeptides which retain substantially the same biological function or activity as the polypeptide characterized by the deduced amino acid sequence of SEQ ID NO.:2. Preferred embodiments in this respect, moreover, are polynucleotides that encode polypeptides that retain substantially the same biological function or activity as the mature polypeptide encoded by the DNA of SEQ ID NO.:1. The present invention further relates to

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polynucleotides that hybridize to the herein above-described sequences. In this regard, the present invention especially relates to polynucleotides that hybridize under stringent conditions to the herein above-described polynucleotides. As herein used, the term "stringent conditions" means hybridization will occur only if there is at least 95% and preferably at least 97% identity between the sequences.

As discussed additionally herein regarding polynucleotide assays of the invention, for instance, polynucleotides of the invention may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding the sequences of SEQ ID NO.:1 and to isolate cDNA and genomic clones of other genes that have a high sequence similarity to SEQ ID NO.:1. Such probes generally will comprise at least 15 bases. Preferably, such probes will have at least 30 bases and may have at least 50 bases. Particularly preferred probes will have at least 30 bases and will have 50 bases or less. For example, the coding region of the gene of the invention may be isolated by screening using the known DNA sequence to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the present invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine to which members of the library the probe hybridizes.

The polypeptides of the present invention include the polypeptide of SEQ ID NO.:2 (in particular the mature polypeptide) as well as polypeptides which have at least 70% identity to the polypeptide of SEQ ID NO.:2, preferably at least 80% identity to the polypeptide of SEQ ID NO.:2, and more preferably at least 90% similarity (more preferably at least 90% identity) to the polypeptide of SEQ ID NO.:2 and still more preferably at least 95% similarity (still more preferably at least 97% identity) to the polypeptide of SEQ ID NO.:2 and also include portions of such polypeptides with such portion of the polypeptide generally containing at least 30 amino acids and more preferably at least 50 amino acids. Representative examples of polypeptide fragments of the invention, include, for example, truncation polypeptides of SEQ ID NO.:2. Truncation polypeptides include polypeptides having the amino acid sequence of SEQ ID NO.:2, or of variants or derivatives thereof, except for

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deletion of a continuous series of residues (that is, a continuous region, part or portion) that includes the amino terminus, or a continuous series of residues that includes the carboxyl terminus or, as in double truncation mutants, deletion of two continuous series of residues, one including the amino terminus and one including the carboxyl terminus. Also preferred in this aspect of the invention are fragments characterized by structural or functional attributes of the polypeptide characterized by the sequences of SEQ ID NO.:2. Preferred embodiments of the invention in this regard include fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, high antigenic index regions of the polypeptide of the invention, and combinations of such fragments. Preferred regions are those that mediate activities of the polypeptides of the invention. Most highly preferred in this regard are fragments that have a chemical, biological or other activity of the response regulator polypeptide of the invention, including those with a similar activity or an improved activity, or with a decreased undesirable activity.

Recombinant expression of protease D-G

The cloned protease D-G DNA obtained through the methods described herein may be recombinantly expressed by molecular cloning into an expression vector containing a suitable promoter and other appropriate transcription regulatory elements, and transferred into prokaryotic or eukaryotic host cells to produce recombinant protease D-G protein. Techniques for such manipulations are fully described in Maniatis, T, *et al.*, *supra*, and are well known in the art.

Expression vectors are defined herein as DNA sequences that are required for the transcription of cloned copies of genes and the translation of their mRNAs in an appropriate host. Such vectors can be used to express eukaryotic genes in a variety of hosts such as bacteria including *E. coli*, bluegreen algae, plant cells, insect cells, fungal cells including yeast cells, and animal cells.

Specifically designed vectors allow the shuttling of DNA between hosts such as bacteria-yeast or bacteria-animal cells or bacteria-fungal cells or bacteria-invertebrate cells. An appropriately constructed expression vector should contain: an origin of replication for autonomous replication in host cells, selectable

10 cloning vectors, specifically designed plasmids or viruses.

15 (Invitrogen), pMC1neo (Stratagene), pXT1 (Stratagene), pSG5 (Stratagene), EBO-pSV2-neo (ATCC 37593) pBPV-1(8-2) (ATCC 37110), pdBPV-MMTneo(342-12) (ATCC 37224), pRSVgpt (ATCC 37199), pRSVneo (ATCC 37198), pSV2-dhfr (ATCC 37146), pUCTag (ATCC 37460), and IZD35 (ATCC 37565).

20 A variety of bacterial expression vectors may be used to express recombinant protease D-G in bacterial cells. Commercially available bacterial expression vectors which may be suitable for recombinant protease D-G expression include, but are not limited to pET vectors (Novagen) and pQE vectors (Qiagen).

25 A variety of fungal cell expression vectors may be used to express recombinant protease D-G in fungal cells such as yeast. Commercially available fungal cell expression vectors which may be suitable for recombinant protease D-G expression include but are not limited to pYES2 (Invitrogen) and Pichia expression vector (Invitrogen).

A variety of insect cell expression vectors may be used to express recombinant protease D-G in insect cells. Commercially available insect cell expression vectors which may be suitable for recombinant expression of protease D-G include but are not limited to pBlueBacII (Invitrogen).

10 limited to drosophila and silkworm derived cell lines.

(ATCC CCL 171), L-cells, and HEK-293 (ATCC CRL1573).

presence of host cell-associated protease D-G activity.

as efficiently translated in cell based systems, including but not limited to

microinjection into frog oocytes, with microinjection into frog oocytes being generally preferred.

20 *Assay methods for protease D-G*

Host cell transfectants and microinjected oocytes may be used to assay both the levels of functional protease D-G activity and levels of total protease D-G protein by the following methods. In the case of recombinant host cells, this involves the co-transfection of one or possibly two or more plasmids, containing the protease D-G DNA encoding one or more fragments encoding the catalytic domain. In the case of oocytes, this involves the co-injection of synthetic RNAs for protease D-G protein. Following an appropriate period of time to allow for expression, cellular protein is metabolically labelled with, for example ^{35}S -methionine for 24 hours, after which cell lysates and cell culture supernatants are

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harvested and subjected to immunoprecipitation with polyclonal antibodies directed against the protease D-G protein.

Levels of protease D-G protein in host cells are quantitated by immunoaffinity and/or proteolytic/amidolytic assay techniques. Cells expressing protease D-G can be assayed for the number of protease D-G molecules expressed by measuring the amount of proteolytic/amidolytic activity. Protease D-G-specific affinity beads or protease D-G-specific antibodies are used to isolate for example ³⁵S-methionine labelled or unlabelled protease D-G protein. Labelled protease D-G protein is analyzed by SDS-PAGE. Unlabelled protease D-G protein is detected by Western blotting, ELISA or RIA assays employing protease D-G specific antibodies.

Cell based assays

The present invention provides a whole cell method to detect compound modulation of protease D-G. The method comprises the steps;

- 1) contacting a compound, and a cell that contains functional protease D-G or purifying functional protease D-G, and
- 2) measuring a change in the cell in response or protease D-G activity by the compound.

The amount of time necessary for protease D-G interaction with the compound is empirically determined, for example, by running a time course with a known protease D-G modulator and measuring cellular/activity changes as a function of time.

The term "cell" refers to at least one cell, but includes a plurality of cells appropriate for the sensitivity of the detection method. Cells suitable for the present invention may be bacterial, yeast, or eukaryotic.

The assay methods to determine compound modulation of functional protease D-G can be in conventional laboratory format or adapted for high throughput. The term "high throughput" refers to an assay design that allows easy analysis of multiple samples simultaneously, and capacity for robotic manipulation. Another desired feature of high throughput assays is an assay

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design that is optimized to reduce reagent usage, or minimize the number of manipulations in order to achieve the analysis desired. Examples of assay formats include 96-well or 384-well plates, levitating droplets, and "lab on a chip" microchannel chips used for liquid handling experiments. It is well known by those in the art that as miniaturization of plastic molds and liquid handling devices are advanced, or as improved assay devices are designed, that greater numbers of samples may be performed using the design of the present invention.

The cellular changes suitable for the method of the present invention comprise directly measuring changes in the function or quantity of protease D-G, or by measuring downstream effects of protease D-G function, for example by measuring secondary messenger concentrations or changes in transcription or by changes in protein levels of genes that are transcriptionally influenced by protease D-G, or by measuring phenotypic changes in the cell. Preferred measurement means include changes in the quantity of protease D-G protein, changes in the functional activity of protease D-G, changes in the quantity of mRNA, changes in intracellular protein, changes in cell surface protein, or secreted protein, or changes in Ca^{+2} , cAMP or GTP concentration. Changes in the quantity or functional activity of protease D-G are described herein. Changes in the levels of mRNA are detected by reverse transcription polymerase chain reaction (RT-PCR) or by differential gene expression. Immunoaffinity, ligand affinity, or enzymatic measurement quantifies changes in levels of protein in host cells. Protein-specific affinity beads or specific antibodies are used to isolate for example ^{35}S -methionine labelled or unlabelled protein. Labelled protein is analyzed by SDS-PAGE. Unlabelled protein is detected by Western blotting, cell surface detection by fluorescent cell sorting, cell image analysis, ELISA or RIA employing specific antibodies. Where the protein is an enzyme, the induction of protein is monitored by cleavage of a fluorogenic or colorimetric substrate.

Preferred detection means for cell surface protein include flow cytometry or statistical cell imaging. In both techniques the protein of interest is localized at the cell surface, labeled with a specific fluorescent probe, and detected via the

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degree of cellular fluorescence. In flow cytometry, the cells are analyzed in a solution, whereas in cellular imaging techniques, a field of cells is compared for relative fluorescence.

A preferred detection means for secreted proteins that are enzymes such as alkaline phosphatase or proteases, would be fluorescent or colorimetric enzymatic assays. Fluorescent/luminescent/color substrates for alkaline phosphatase are commercially available and such assays are easily adaptable to high throughput multiwell plate screen format. Fluorescent energy transfer based assays are used for protease assays. Fluorophore and quencher molecules are incorporated into the two ends of the peptide substrate of the protease. Upon cleavage of the specific substrate, separation of the fluorophore and quencher allows the fluorescence to be detectable. When the secreted protein could be measure by radioactive methods, scintillation proximity technology could be used. The substrate of the protein of interest is immobilized either by coating or incorporation on a solid support that contains a fluorescent material. A radioactive molecule, brought in close proximity to the solid phase by enzyme reaction, causes the fluorescent material to become excited and emit visible light. Emission of visible light forms the basis of detection of successful ligand/target interaction, and is measured by an appropriate monitoring device. An example of a scintillation proximity assay is disclosed in United States Patent No. 4,568,649, issued February 4, 1986. Materials for these types of assays are commercially available from Dupont NEN® (Boston, Massachusetts) under the trade name FlashPlate™.

A preferred detection means where the endogenous gene results in phenotypic cellular structural changes is statistical image analysis the cellular morphology or intracellular phenotypic changes. For example, but not by way of limitation, and cell may change morphology such a rounding versus remaining flat against a surface, or may become growth-surface independent and thus resemble transformed cell phenotype well known in the art of tumor cell biology, or a cell may produce new outgrowths. Phenotypic changes that may occur intracellularly

include cytoskeletal changes, alteration in the entoplasmic reticulum/Golgi complex in response to new gene transcription, or production of new vesicles.

5 protein contained within the cell lysate. The soluble protein may be measured by the methods described herein.

as well as the function of protease D-G protein *in vivo*. Compounds may modulate by increasing or attenuating the expression of DNA or RNA encoding protease D-G, or the function of protease D-G protein. Compounds that modulate the expression of DNA or RNA encoding protease D-G or the function of protease D-G protein may be detected by a variety of assays. The assay may be a simple "yes/no" assay to determine whether there is a change in expression or function. The assay may be made quantitative by comparing the expression or function of a test sample with the levels of expression or function in a standard sample. Modulators identified in this process are useful as therapeutic agents, and protease D-G.

20

Purification of protease D-G protein

25 (add references for purification of similar proteins that could be the basis of a
purification scheme). As described above for purification of protease D-G from
natural sources, recombinant protease D-G may be purified from cell lysates and
extracts, or from conditioned culture medium, by various combinations of, or
individual application of salt fractionation, ion exchange chromatography, size
30 exclusion chromatography, hydroxylapatite adsorption chromatography and

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hydrophobic interaction chromatography, lectin chromatography, and antibody/ligand affinity chromatography.

Recombinant protease D-G can be separated from other cellular proteins by use of an immunoaffinity column made with monoclonal or polyclonal antibodies specific for full length nascent protease D-G, polypeptide fragments of protease D-G or protease D-G subunits. The affinity resin is then equilibrated in a suitable buffer, for example phosphate buffered saline (pH 7.3), and the cell culture supernatants or cell extracts containing protease D-G or protease D-G subunits are slowly passed through the column. The column is then washed with the buffer until the optical density (A_{280}) falls to background, then the protein is eluted by changing the buffer condition, such as by lowering the pH using a buffer such as 0.23 M glycine-HCl (pH 2.6). The purified protease D-G protein is then dialyzed against a suitable buffer such as phosphate buffered saline.

Protein based assay

The present invention provides an *in vitro* protein assay method to detect compound modulation of protease D-G protein activity. The method comprises the steps;

- 1) contacting a compound, and function protease D-G protein, and
- 2) measuring a change to protease D-G function by the compound.

The amount of time necessary for cellular contact with the compound is empirically determined, for example, by running a time course with a known protease D-G modulator and measuring changes as a function of time.

this section is directed to protease assays

Methods for detecting compounds that modulate protease D-G proteolytic activity comprise combining a punitive modulating compound, functional protease D-G protein, and a suitable labeled substrate and monitoring an effect of the compound on the protease by changes in the amount of substrate either as a function of time or after a predefined period of time. Labeled substrates include, but are not limited to; substrate that is radiolabeled (Coolican et al. (1986). *J. Biol. Chem.* 261:4170-6),

fluorometric (Lonergan et al. (1995). *J. Food Sci.* 60:72-3, 78; Twining (1984). *Anal. Biochem.* 143:30-4) or colorimetric (Buroker-Kilgore and Wang (1993). *Anal. Biochem.* 208:387-92). Radioisotopes useful for use in the present invention include those well known in the art, specifically ^{125}I , ^{131}I , ^3H , ^{14}C , ^{35}S , ^{32}P , and ^{33}P .

- A preferred assay format useful for the method of the present invention is a FRET based method using peptide substrates that contain a fluorescent donor with either a quencher or acceptor that are separated by a peptide sequence encoding the protease D-G cleavage site. A fluorescent donor is a fluorogenic compound that can adsorb energy and transfers a portion of the energy to another compound. Examples of fluorescent donors suitable for use in the present invention include, but are not limited to, coumarins, xanthene dyes such as fluoresceins, rhodols, and rhodamines, resorufins, cyanine dyes bimanes, acridines, isoindols, dansyl dyes, aminophthalic hydrazides such as luminol and isoluminol derivatices, aminophthalimides, aminonaphthalimides, aminobenzofurans, aminoquinolines, dicanohydroquinones, and europium and terbium complexes and related compounds. A quencher is a compound that reduces the emission from the fluorescent donor when it is appropriately proximally located to the donor, and do not generally re-emit the energy in the form of fluorescence. Examples of such moieties include indigos, bezoquinones,

A preferred assay format useful for the method of the present invention is a FRET based method using peptide substrates that contain a fluorescent donor with either a quencher or acceptor that are separated by a peptide sequence encoding the protease D-G cleavage site. A fluorescent donor is a fluorogenic compound that can adsorb energy and transfers a portion of the energy to another compound. Examples of fluorescent donors suitable for use in the present invention include, but are not limited to, coumarins, xanthene dyes such as fluoresceins, rhodols, and rhodamines, resorufins, cyanine dyes bimanes, acridines, isoindols, dansyl dyes, aminophthalic hydrazides such as luminol and isoluminol derivatices, aminophthalimides, aminonaphthalimides, aminobenzofurans, aminoquinolines, dicanohydroquinones, and europium and terbium complexes and related compounds. A quencher is a compound that reduces the emission from the fluorescent donor when it is appropriately proximally located to the donor, and do not generally re-emit the energy in the form of fluorescence. Examples of such moieties include indigos, bezoquinones,

anthraquinones, azo compounds, nitro compounds, indoanilines, and di- and triphenylmethanes. A FRET method using a donor/quencher pair measures increased emission from the fluorescent donor as a function of protease D-G enzymatic activity upon the peptide substrate. Therefore a test compound th

10 An acceptor is a specific type of quencher that enables a separate mechanism to measure protease D-G proteolytic efficacy. Methods that utilize a donor/acceptor pair measure a decrease in acceptor emission as a function of protease D-G enzymatic activity upon the peptide substrate. Therefore a test compound that antagonizes protease D-G will generate an emission signal between two control
15 samples – a higher basal fluorescence from the FRET peptide alone and a lower fluorescence from the FRET peptide digested by the activity of enzymatically active protease D-G. Examples of acceptor useful for methods of the present invention include, but are not limited to, coumarins, fluoresceins, rhodols, rhodamines, resorufins, cyanines, difluoroboradiazindacenes, and phthalcyanines.

Monospecific antibodies to protease D-G are purified from mammalian antisera containing antibodies reactive against protease D-G or are prepared as monoclonal antibodies reactive with protease D-G using the technique originally described by Kohler and Milstein, *Nature* 256: 495-497 (1975). Immunological techniques are well known in the art and described in, for example, Antibodies: A laboratory manual published by Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, ISBN 0879693142. Monospecific antibody as used herein is defined as a single antibody species or multiple antibody species with homogenous binding characteristics for protease D-G. Homogenous binding as

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used herein refers to the ability of the antibody species to bind to a specific antigen or epitope, such as those associated with the protease D-G, as described above. protease D-G specific antibodies are raised by immunizing animals such as mice, rats, guinea pigs, rabbits, goats, horses and the like, with rabbits being
5 preferred, with an appropriate concentration of protease D-G either with or without an immune adjuvant.

Preimmune serum is collected prior to the first immunization. Each animal receives between about 0.001 mg and about 1000 mg of protease D-G associated with an acceptable immune adjuvant. Such acceptable adjuvants
10 include, but are not limited to, Freund's complete, Freund's incomplete, alum-precipitate, water in oil emulsion containing Corynebacterium parvum and tRNA. The initial immunization consists of protease D-G in, preferably, Freund's complete adjuvant at multiple sites either subcutaneously (SC), intraperitoneally (IP) or both. Each animal is bled at regular intervals, preferably weekly, to
15 determine antibody titer. The animals may or may not receive booster injections following the initial immunization. Those animals receiving booster injections are generally given an equal amount of the antigen in Freund's incomplete adjuvant by the same route. Booster injections are given at about three-week intervals until maximal titers are obtained. At about 7 days after each booster
20 immunization or about weekly after a single immunization, the animals are bled, the serum collected, and aliquots are stored at about -20°C.

Monoclonal antibodies (mAb) reactive with protease D-G are prepared by immunizing inbred mice, preferably Balb/c, with protease D-G. The mice are immunized by the IP or SC route with about 0.001 mg to about 1.0 mg, preferably
25 about 0.1 mg, of protease D-G in about 0.1 ml buffer or saline incorporated in an equal volume of an acceptable adjuvant, as discussed above. Freund's adjuvant is preferred, with Freund's complete adjuvant being used for the initial immunization and Freund's incomplete adjuvant used thereafter. The mice receive an initial immunization on day 0 and are rested for about 2 to about 30
30 weeks. Immunized mice are given one or more booster immunizations of about

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0.001 to about 1.0 mg of protease D-G in a buffer solution such as phosphate buffered saline by the intravenous (IV) route. Lymphocytes, from antibody positive mice, preferably splenic lymphocytes, are obtained by removing spleens from immunized mice by standard procedures known in the art. Hybridoma cells
5 are produced by mixing the splenic lymphocytes with an appropriate fusion partner, preferably myeloma cells, under conditions that will allow the formation of stable hybridomas. Fusion partners may include, but are not limited to: mouse myelomas P3/NS1/Ag 4-1; MPC-11; S-194 and Sp2/0, with Sp2/0 being generally preferred. The antibody producing cells and myeloma cells are fused in
10 polyethylene glycol, about 1000 mol. wt., at concentrations from about 30% to about 50%. Fused hybridoma cells are selected by growth in hypoxanthine, thymidine and aminopterin supplemented Dulbecco's Modified Eagles Medium (DMEM) by procedures known in the art. Supernatant fluids are collected from growth positive wells on about days 14, 18, and 21 and are screened for antibody
15 production by an immunoassay such as solid phase immunoradioassay (SPIRA) using protease D-G as the antigen. The culture fluids are also tested in the Ouchterlony precipitation assay to determine the isotype of the mAb. Hybridoma cells from antibody positive wells are cloned by a technique such as the soft agar technique of MacPherson, Soft Agar Techniques, in Tissue Culture Methods and
20 Applications, Kruse and Paterson, Eds., Academic Press, 1973 or by the technique of limited dilution.

Monoclonal antibodies are produced *in vivo* by injection of pristane primed Balb/c mice, approximately 0.5 ml per mouse, with about 1×10^6 to about 6×10^6 hybridoma cells at least about 4 days after priming. Ascites fluid is
25 collected at approximately 8-12 days after cell transfer and the monoclonal antibodies are purified by techniques known in the art.

In vitro production of anti-protease D-G mAb is carried out by growing the hybridoma in tissue culture media well known in the art. High density *in vitro* cell culture may be conducted to produce large quantities of anti-protease D-G
30 mAbs using hollow fiber culture techniques, air lift reactors, roller bottle, or

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spinner flasks culture techniques well known in the art. The mAb are purified by techniques known in the art.

Antibody titers of ascites or hybridoma culture fluids are determined by various serological or immunological assays which include, but are not limited to, precipitation, passive agglutination, enzyme-linked immunosorbent antibody (ELISA) technique and radioimmunoassay (RIA) techniques. Similar assays are used to detect the presence of protease D-G in body fluids or tissue and cell extracts.

It is readily apparent to those skilled in the art that the above described methods for producing monospecific antibodies may be utilized to produce antibodies specific for protease D-G polypeptide fragments, or full-length nascent protease D-G polypeptide, or the individual protease D-G subunits. Specifically, it is readily apparent to those skilled in the art that monospecific antibodies may be generated which are specific for only one protease D-G subunit or the fully functional protease D-G protein. It is also apparent to those skilled in the art that monospecific antibodies may be generated that inhibit normal function of protease D-G protein.

Protease D-G antibody affinity columns are made by adding the antibodies to a gel support such that the antibodies form covalent linkages with the gel bead support. Preferred covalent linkages are made through amine, aldehyde, or sulfhydryl residues contained on the antibody. Methods to generate aldehydes or free sulfhydryl groups on antibodies are well known in the art; amine groups are reactive with, for example, N-hydroxysuccinimide esters.

The aberrant expression or regulation of proteolytic activity can result in numerous pathophysiological states. For example several bleeding disorders, resulting from genetic lesions, are known to be caused by the deficiency in any one of a number of active serine protease coagulation factors. Many cancerous cells and tumors over-express proteases, several of which have been identified as serine proteases. These enzymes are thought to facilitate tumor growth and/or

5 extracellular matrix degradation or by the specific activation of pro-hormone precursors into active growth regulators or chemoattractants. Thus it is easy to imagine how modulators of serine protease activity could have profound effects of various pathophysiological conditions.

10 *Kit compositions containing protease D-G specific reagents*

Kits containing protease D-G DNA or RNA, antibodies to protease D-G, or protease D-G protein may be prepared. Such kits are used to detect DNA which hybridizes to protease D-G DNA or to detect the presence of protease D-G protein or peptide fragments in a sample. Such characterization is useful for a variety of purposes including but not limited to forensic analyses, diagnostic applications, and epidemiological studies.

The DNA molecules, RNA molecules, recombinant protein and antibodies of the present invention may be used to screen and measure levels of protease D-G DNA, protease D-G RNA or protease D-G protein. The recombinant proteins, DNA molecules, RNA molecules and antibodies lend themselves to the formulation of kits suitable for the detection and typing of protease D-G. Such a kit would comprise a compartmentalized carrier suitable to hold in close confinement at least one container. The carrier would further comprise reagents such as recombinant protease D-G protein or anti-protease D-G antibodies suitable for detecting protease D-G. The carrier may also contain a means for detection such as labeled antigen or enzyme substrates or the like.

Gene therapy

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Nucleotide sequences that are complementary to the protease D-G encoding DNA sequence can be synthesized for antisense therapy. These antisense molecules may be DNA, stable derivatives of DNA such as phosphorothioates or methylphosphonates, RNA, stable derivatives of RNA such as 2'-O-alkylRNA, or other protease D-G antisense oligonucleotide mimetics. protease D-G antisense molecules may be introduced into cells by microinjection, liposome encapsulation or by expression from vectors harboring the antisense sequence. protease D-G antisense therapy may be particularly useful for the treatment of diseases where it is beneficial to reduce protease D-G activity.

protease D-G gene therapy may be used to introduce protease D-G into the cells of target organisms. The protease D-G gene can be ligated into viral vectors that mediate transfer of the protease D-G DNA by infection of recipient host cells. Suitable viral vectors include retrovirus, adenovirus, adeno-associated virus, herpes virus, vaccinia virus, polio virus and the like. Alternatively, protease D-G DNA can be transferred into cells for gene therapy by non-viral techniques including receptor-mediated targeted DNA transfer using ligand-DNA conjugates or adenovirus-ligand-DNA conjugates, lipofection membrane fusion or direct microinjection. These procedures and variations thereof are suitable for *ex vivo* as well as *in vivo* protease D-G gene therapy. protease D-G gene therapy may be particularly useful for the treatment of diseases where it is beneficial to elevate protease D-G activity. Protocols for molecular methodology of gene therapy suitable for use with the protease D-G gene is described in Gene Therapy Protocols, edited by Paul D. Robbins, Human press, Totawa NJ, 1996.

25 *Pharmaceutical compositions*

Pharmaceutically useful compositions comprising protease D-G DNA, protease D-G RNA, or protease D-G protein, or modulators of protease D-G receptor activity, may be formulated according to known methods such as by the admixture of a pharmaceutically acceptable carrier. Examples of such carriers and methods of formulation may be found in Remington's Pharmaceutical

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Sciences. To form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of the protein, DNA, RNA, or modulator.

Therapeutic or diagnostic compositions of the invention are administered to an individual in amounts sufficient to treat or diagnose disorders in which modulation of protease D-G-related activity is indicated. The effective amount may vary according to a variety of factors such as the individual's condition, weight, sex and age. Other factors include the mode of administration. The pharmaceutical compositions may be provided to the individual by a variety of routes such as subcutaneous, topical, oral and intramuscular.

The term "chemical derivative" describes a molecule that contains additional chemical moieties that are not normally a part of the base molecule. Such moieties may improve the solubility, half-life, absorption, etc. of the base molecule. Alternatively the moieties may attenuate undesirable side effects of the base molecule or decrease the toxicity of the base molecule. Examples of such moieties are described in a variety of texts, such as Remington's Pharmaceutical Sciences.

Compounds identified according to the methods disclosed herein may be used alone at appropriate dosages defined by routine testing in order to obtain optimal inhibition of the protease D-G receptor or its activity while minimizing any potential toxicity. In addition, co-administration or sequential administration of other agents may be desirable.

The present invention also has the objective of providing suitable topical, oral, systemic and parenteral pharmaceutical formulations for use in the novel methods of treatment of the present invention. The compositions containing compounds or modulators identified according to this invention as the active ingredient for use in the modulation of protease D-G can be administered in a wide variety of therapeutic dosage forms in conventional vehicles for administration. For example, the compounds or modulators can be administered in such oral dosage forms as tablets, capsules (each including timed release and

sustained release formulations), pills, powders, granules, elixirs, tinctures, solutions, suspensions, syrups and emulsions, or by injection. Likewise, they may also be administered in intravenous (both bolus and infusion), intraperitoneal, subcutaneous, topical with or without occlusion, or intramuscular form, all using forms well known to those of ordinary skill in the pharmaceutical arts. An effective but non-toxic amount of the compound desired can be employed as a protease D-G modulating agent.

Advantageously, compounds or modulators of the present invention may be administered in a single daily dose, or the total daily dosage may be administered in divided doses of two, three or four times daily. Furthermore, compounds or modulators for the present invention can be administered in intranasal form via topical use of suitable intranasal vehicles, or via transdermal routes, using those forms of transdermal skin patches well known to those of ordinary skill in that art. To be administered in the form of a transdermal delivery system, the dosage administration will, of course, be continuous rather than intermittent throughout the dosage regimen.

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For combination treatment with more than one active agent, where the active agents are in separate dosage formulations, the active agents can be administered concurrently, or they each can be administered at separately staggered times.

- 5 The dosage regimen utilizing the compounds or modulators of the present invention is selected in accordance with a variety of factors including type, species, age, weight, sex and medical condition of the patient; the severity of the condition to be treated; the route of administration; the renal and hepatic function of the patient; and the particular compound thereof employed. A physician or
10 veterinarian of ordinary skill can readily determine and prescribe the effective amount of the drug required to prevent, counter or arrest the progress of the condition. Optimal precision in achieving concentrations of drug within the range that yields efficacy without toxicity requires a regimen based on the kinetics of the drug's availability to target sites. This involves a consideration of the
15 distribution, equilibrium, and elimination of a drug.

- In the methods of the present invention, the compounds or modulators herein described in detail can form the active ingredient, and are typically administered in admixture with suitable pharmaceutical diluents, excipients or carriers (collectively referred to herein as "carrier" materials) suitably selected
20 with respect to the intended form of administration, that is, oral tablets, capsules, elixirs, syrups and the like, and consistent with conventional pharmaceutical practices.

- For instance, for oral administration in the form of a tablet or capsule, the active drug component can be combined with an oral, non-toxic pharmaceutically
25 acceptable inert carrier such as ethanol, glycerol, water and the like. Moreover, when desired or necessary, suitable binders, lubricants, disintegrating agents and coloring agents can also be incorporated into the mixture. Suitable binders include, without limitation, starch, gelatin, natural sugars such as glucose or beta-lactose, corn sweeteners, natural and synthetic gums such as acacia, tragacanth or
30 sodium alginate, carboxymethylcellulose, polyethylene glycol, waxes and the like.

Lubricants used in these dosage forms include, without limitation, sodium oleate, sodium stearate, magnesium stearate, sodium benzoate, sodium acetate, sodium chloride and the like. Disintegrators include, without limitation, starch, methyl cellulose, agar, bentonite, xanthan gum and the like.

5 For liquid forms the active drug component can be combined in suitably flavored suspending or dispersing agents such as the synthetic and natural gums, for example, tragacanth, acacia, methyl-cellulose and the like. Other dispersing agents that may be employed include glycerin and the like. For parenteral administration, sterile suspensions and solutions are desired. Isotonic preparations, which generally
10 contain suitable preservatives, are employed when intravenous administration is desired.

Topical preparations containing the active drug component can be admixed with a variety of carrier materials well known in the art, such as, e.g., alcohols, aloe vera gel, allantoin, glycerine, vitamin A and E oils, mineral oil, PPG2 myristyl propionate, and the like, to form, e.g., alcoholic solutions, topical cleansers, cleansing
15 creams, skin gels, skin lotions, and shampoos in cream or gel formulations.

The compounds or modulators of the present invention can also be administered in the form of liposome delivery systems, such as small unilamellar vesicles, large unilamellar vesicles and multilamellar vesicles. Liposomes can be formed from a variety of phospholipids, such as cholesterol, stearylamine or phosphatidylcholines.

Compounds of the present invention may also be delivered by the use of monoclonal antibodies as individual carriers to which the compound molecules are coupled. The compounds or modulators of the present invention may also be coupled with soluble polymers as targetable drug carriers. Such polymers can include polyvinyl-pyrrolidone, pyran copolymer, polyhydroxypropylmethacryl-
amidephenol, polyhydroxy-ethylaspartamidephenol, or polyethyl-
eneoxidepolylysine substituted with palmitoyl residues. Furthermore, the compounds or modulators of the present invention may be coupled to a class of
biodegradable polymers useful in achieving controlled release of a drug, for

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example, polylactic acid, polyepsilon caprolactone, polyhydroxy butyric acid, polyorthoesters, polyacetals, polydihydro-pyrans, polycyanoacrylates and cross-linked or amphipathic block copolymers of hydrogels.

For oral administration, the compounds or modulators may be administered in capsule, tablet, or bolus form or alternatively they can be mixed in the animals feed. The capsules, tablets, and boluses are comprised of the active ingredient in combination with an appropriate carrier vehicle such as starch, talc, magnesium stearate, or di-calcium phosphate. These unit dosage forms are prepared by intimately mixing the active ingredient with suitable finely-powdered inert ingredients including diluents, fillers, disintegrating agents, and/or binders such that a uniform mixture is obtained. An inert ingredient is one that will not react with the compounds or modulators and which is non-toxic to the animal being treated. Suitable inert ingredients include starch, lactose, talc, magnesium stearate, vegetable gums and oils, and the like. These formulations may contain a widely variable amount of the active and inactive ingredients depending on numerous factors such as the size and type of the animal species to be treated and the type and severity of the infection. The active ingredient may also be administered as an additive to the feed by simply mixing the compound with the feedstuff or by applying the compound to the surface of the feed. Alternatively the active ingredient may be mixed with an inert carrier and the resulting composition may then either be mixed with the feed or fed directly to the animal. Suitable inert carriers include corn meal, citrus meal, fermentation residues, soya grits, dried grains and the like. The active ingredients are intimately mixed with these inert carriers by grinding, stirring, milling, or tumbling such that the final composition contains from 0.001 to 5% by weight of the active ingredient.

The compounds or modulators may alternatively be administered parenterally via injection of a formulation consisting of the active ingredient dissolved in an inert liquid carrier. Injection may be either intramuscular,

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intraruminal, intratracheal, or subcutaneous. The injectable formulation consists of the active ingredient mixed with an appropriate inert liquid carrier. Acceptable liquid carriers include the vegetable oils such as peanut oil, cotton seed oil, sesame oil and the like as well as organic solvents such as solketal, glycerol formal and the like. As an alternative, aqueous parenteral formulations may also be used. The vegetable oils are the preferred liquid carriers. The formulations are prepared by dissolving or suspending the active ingredient in the liquid carrier such that the final formulation contains from 0.005 to 10% by weight of the active ingredient.

Topical application of the compounds or modulators is possible through the use of a liquid drench or a shampoo containing the instant compounds or modulators as an aqueous solution or suspension. These formulations generally contain a suspending agent such as bentonite and normally will also contain an antifoaming agent. Formulations containing from 0.005 to 10% by weight of the active ingredient are acceptable. Preferred formulations are those containing from 0.01 to 5% by weight of the instant compounds or modulators.

The following examples illustrate the present invention without, however, limiting the same thereto.

EXAMPLE 1

Plasmid Manipulations

All molecular biological methods were in accordance with those previously described (Maniatis et al. (1989). 1-1626). Oligonucleotides were purchased from Ransom Hill Biosciences (Ransom Hill, CA) and all restriction endonucleases and other DNA modifying enzymes were from New England Biolabs (Beverly, MA) unless otherwise specified. The protease D-G expression construct was made in the baculovirus expression vector pFastBac1 (Life Technologies, Gaithersburg, MD) as described below. All construct

manipulations were confirmed by dye terminator cycle sequencing using Allied Biosystems 377 fluorescent sequencers (Perkin Elmer, Foster City, CA).

Acquisition of Protease D-G cDNA

A recombinant phage containing the protease D-G cDNA was isolated from a human small intestine library (Clontech, Palo Alto, CA). The insert was subjected to sequence analysis and it was found to contain an open reading frame of 1305 nucleotides excluding the TAA stop codon (SEQ ID NO.:1), which had homology to S1 serine proteases. Significantly, the open reading frame is likely to be authentic since it is preceded by an in-frame TGA stop codon at position 157. This clone is also likely to contain the entire 3' untranslated since a putative polyadenylation sequence (ATTAAA) with a good match to the known sequence was (AATAAA) was also identified just upstream of a poly A stretch. The deduced open reading frame encodes a preproD-G protein of 435 amino acids (SEQ ID NO.:2), with an estimated molecular mass (M_r) of about 48-Kd, and a strong homology to other serine proteases. Additional sequence analysis of the protease D-G amino acid sequence predicted a transmembrane segment near the amino terminus (residues 31-52 in SEQ ID NO.:2), suggesting that this novel cDNA encoded a type II transmembrane serine protease. Homology searches of the Genbank database with the protease D-G cDNA indicated that this was a novel cDNA had closest similarity to the cloned serine proteases TMPRSS2 (Paoloni-Giacobino et al. (1997). *Genomics* 44:309-320) and hepsin (Leytus et al. (1988). *Biochemistry* 27:1067-74), which are also type II integral membrane proteases. The zymogen activation sequence is very similar to that of other S1 serine proteases and predicts a mature protein of 233 amino acids. The catalytic triad residues H, D and S of protease D-G are located at positions 243, 339 and 385, respectively (using the methionine initiator of the prepro D-G sequence as number one). A phylogenetic tree of the deduced protease D-G amino acid sequence with other members of the S1 serine protease family was generated by the Clustal W program (Higgins and Sharp (1989). *Comput. Appl. Biosci.* 5:151-3) shown in Figure 2 as determined using the MegAlign 3.1.7 program (DNASTAR Inc., Madison, WI).

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EXAMPLE 2*Tissue Distribution of The Protease D-G mRNA*

We employed a highly sensitive PCR profiling technique to identify the tissue distribution of protease D-G mRNA. For this application, several human cDNA libraries (all were from Clontech, (Palo Alto, CA) except the CHRF-288 megakaryocytic cell line and human gel filtered platelet libraries which we constructed using the ZAP Express cDNA system (Stratagene, La Jolla, CA). The PCR primers for the profiling analysis were as follows:

10 SEQ.ID.NO.3: 5'- ACAGCCTCAGCATTTCTTGG -3'

 SEQ.ID.NO.4: 5'- TCTTGCTCTAGTAGGCTTGG -3'

Briefly, the 50 μ l PCR reactions used 1 μ l of diluted phage stock ($\sim 10^8$ to 10^{10} pfu/ml) from each of the cDNA libraries tested. Reactions were initially denatured at 94 °C for 5 min. and subjected to 35 cycles of 94 °C for 20 sec.; 56 °C for 20 sec.; and then 72 °C for 30 sec. followed by a final 72 °C elongation for 10 min. A nested primer probe of the sequence

SEQ.ID.NO.5: 5'-

TTGGTGCTCCCAGCATCCCAGGGAGAGACACAGCCCACTG -3' was

radiolabeled using gamma 32 P-ATP and T4 polynucleotide kinase (Life Technologies, Gaithersberg, MD) and unincorporated label was removed, following the reaction, using a QIAquick nucleotide removal column (Qiagen, Valencia, CA). The 32 P end-labeled nested primer probe (1×10^5 cpm) was combined with 10 μ l of each sample following the PCR reaction. The PCR product-probe mixtures were denatured at 94 °C for 5 min.; hybridized at 60 °C for 15 minutes, and cooled to 4 °C. The annealed samples (10 μ l) were electrophoresed in 6% Tris-Borate-EDTA non-denaturing polyacrylamide gels (Novex), dried and exposed by autoradiography. A PCR profile of the cDNA libraries used in Figure 3 with beta-actin PCR primers and labeled nested primer probe produced a beta-actin PCR product in all samples examined.

As seen in Figure 3, the distribution of protease D-G mRNA is highly restricted to specific tissues and cell types. The tissue types expressing the protease

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D-G transcript are epidermis, fibroblasts, keratinocytes, colon, small intestine, stomach, lung, kidney, bone marrow, lymph node, thymus, ovary, prostate, uterus and spinal cord. Of particular significance is that D-G protease mRNA is not expressed in pancreas or liver, tissues normally found to express numerous serine protease genes.

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EXAMPLE 3

Construct Generation For The Expression of Active Protease D-G

Since members of the S1 protease family are most often synthesized as inactive zymogen precursors, and require limited proteolysis to become

10 proteolytically active, we have developed a zymogen activation construct to express and permit the generic activation of heterologous serine protease cDNAs. This construct features a bovine preprolactin signal sequence fused in-frame with the MoAb M2 anti-FLAG antibody epitope as previously described (Ishii et al. (1993). *J. Biol. Chem.* 268:9780-6) for the purposes of secretion and antibody

15 detection respectively (PF). Significantly, this construct also contains the enterokinase cleavage site from human trypsinogen I (EK) fused in-frame and downstream from the signal sequence. At the C-terminus, preceding a stop codon, is an additional sequence encoding 6 histidine (6XHIS) codons for affinity purification on nickel resins respectively. A unique Xba I restriction enzyme site,

20 immediately upstream of the affinity tag sequence and downstream of the PFEK prepro sequence described above, and is the point of in-frame insertion of the catalytic domain of a heterologous serine protease cDNA (Figure 4). The zymogen activation vector described above has been cloned into a modified pFastBac1 transplacement plasmid to generate PFEK-6XHIS-TAG FB.

25 The purified plasmid DNA of the full length protease D-G cDNA was used as a template in a 100 µl preparative PCR reaction using the Native Pfu Polymerase (Stratagene, La Jolla, CA) in accordance with the manufacturer's recommendations. The primers used

SEQ.ID.NO.6: D-G Xba-U 5'- ATGCTCTAGATGTGGATTCTTGGCCTTGGC
30 -3' SEQ.ID.NO.7: D-G Xba-L 5'-

GATGTCTAGACAGCTCAGCCTTCCAGACATTG -3' contained Xba I cleavable ends, and were designed to flank the catalytic domain of protease D-G and generate the protease D-G Xba I catalytic cassette. The preparative PCR reaction was run at 18 cycles of 94 °C for 30 sec.; 60 °C for 30 sec; 72 °C for 2.0 min.

The preparative PCR product was phenol/CHCl₃ (1:1) extracted once, CHCl₃ extracted, and then EtOH precipitated with glycogen (Boehringer Mannheim Corp., Indianapolis, IN) and carrier. The precipitated pellet was rinsed with 70 % EtOH, dried by vacuum, and resuspended in 80 ul H₂O, 10 ul 10 restriction buffer number 2 and 1 ul 100x BSA (New England Biolabs, Beverly, MA). The product was digested for 3 hr. at 37 °C with 200 units Xba I restriction enzyme (New England Biolabs, Beverly, MA). The Xba I digested product was phenol/CHCl₃ (1:1) extracted once, CHCl₃ extracted, EtOH precipitated, rinsed with 70 % EtOH, and dried by vacuum. For purification from contaminating template plasmid DNA, the product was electrophoresed through 1.0 % low melting temperature agarose (Life Technologies, Gaithersburg, MD) gels in TAE buffer (40 mM Tris-Acetate, 1 mM EDTA pH 8.3) and excised from the gel. An aliquot of the excised product was then used for in-gel ligations with the Xba I digested, dephosphorylated and gel purified, zymogen activation vector described above. Clones containing the D-G Xba cassette, inserted in the correct orientation to generate the construct PFEK-protease D-G-6XHIS-TAG 64, were confirmed by sequence analyses to ensure that the proper translational register with respect to the NH₂-terminal PFEK prepro sequence and C-terminal 6XHIS affinity tag was maintained.

Expression of Recombinant Protease D-G

The recombinant bacmid containing the PFEK-protease D-G-6XHIS construct was prepared from bacterial transformation, selection, growth, purification and PCR confirmation in accordance with the manufacturer's recommendations.

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Cultured Sf9 insect cells (ATCC CRL-1711) were transfected with purified bacmid DNA and several days later, conditioned media containing recombinant PFEK- protease D-G-6XHIS baculovirus was collected for viral stock amplification. Sf9 cells growing in Sf-900 II SFM at a density of 2×10^6 /ml were infected at a multiplicity of infection of 2 at 27 °C for 80 hours, and media was collected and concentrated for purification of PFEK- protease D-G-6XHIS.

EXAMPLE 5

Purification, and Activation of Recombinant Protease D-G

Culture supernatants from baculovirus infected Sf9 cells expressing PFEK-D-G-6XHIS were concentrated and desalted at 4 °C using a Centricon Plus-80 Biomax-8 concentrator (Millipore, Marlborough, MA). Ni-NTA (150 µl of a 50 % slurry/per 100 µg of zymogen) (Qiagen, Valencia, CA) was added to 5 ml the concentrated sample and mixed by shaking at 4 °C for 60 min. The zymogen-bound resin was washed 3 times with wash buffer [10 mM Tris-HCl (pH 8.0), 300 mM NaCl, and 15 mM imidazole], followed by with a 1.5 ml wash with ds H₂O. Zymogen cleavage was carried out by adding enterokinase (10 U per 50 µg of zymogen) (Novagen, Inc., Madison WI; or Sigma, St. Louis, MO) to the zymogen-bound Ni-NTA beads in a small volume at room temperature overnight with gentle shaking in a buffer containing 20 mM Tris-HCl (pH 7.4), 50 mM NaCl, and 2.0 mM CaCl₂. The resin was then washed twice with 1.5 ml wash buffer. The activated protease D-G-6XHIS was eluted with elution buffer [20 mM Tris-HCl (pH 7.8), 250 mM NaCl, and 250 mM imidazole]. Eluted protein concentration was determined by a Micro BCA Kit (Pierce, Rockford, IL) using bovine serum albumin as a standard.

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Electrophoresis and Western Blotting Detection of Recombinant Proteases D-G

Samples of the purified PFEK-protease D-G-6XHIS zymogen or activated protease D-G-6XHIS, denatured in the presence of the reducing agent dithiothreitol (DTT), were analyzed by SDS-PAGE (Bio Rad, Hercules CA) stained with Coomassie Brilliant Blue. For Western blotting, gels were electrotransferred to

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Hybond ECL membranes (Amersham, Arlington Heights, IL). The FLAG-tagged PFEK-protease D-G-6XHis zymogen expressed from infected Sf9 cells was detected with anti-Flag M2 antibody (Babco, Richmond, CA). The secondary antibody was a goat-anti-mouse IgG (H+L), horseradish peroxidase-linked F(ab')₂ fragment, (Boehringer Mannheim Corp., Indianapolis, IN) and was detected by the ECL kit (Amersham, Arlington Heights, IL).

Chromogenic Assay of Activated Recombinant Proteases D-G

Amidolytic activities of the activated serine proteases are monitored by release of para-nitroaniline (pNA) from synthetic substrates that are commercially available (Bachem California Inc., Torrance, PA; American Diagnostica Inc., Greenwich, CT; Kabi Pharmacia Hepar Inc., Franklin, OH). Assay mixtures contain chromogenic substrates in 500 μ M and 10 mM TRIS-HCl (pH 7.8), 25 mM NaCl, and 25 mM imidazole. Release of pNA is measured over 120 min at 37 °C on a micro-plate reader (Molecular Devices, Menlo Park, CA) with a 405 nm absorbance filter. The initial reaction rates (V_{max} , mOD/min) are determined from plots of absorbance versus time using Softmax (Molecular Devices, Menlo Park, CA). The specific activities (nmole pNA produced /min/ μ g protein) of the activated protease D-G-6XHIS for the various substrates are presented in Table 1. No measurable chromogenic amidolytic activity was detected with the purified unactivated PFEK-protease D-G-6XHIS zymogen.

TABLE 1
SPECIFIC ACTIVITY TABLE

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Chromogenic Substrates	Specific Activity
H-D-Pro-HHT-Arg-pNA	0.046±0.001
H-D-Lys(CBO)-Pro-Arg-pNA	0.076±0.008
Z-Phe-Arg-pNA	0.116±0.006
H-D-Val-Leu-Arg-pNA	0.025±0.003
H-D-Val-Leu-Lys-pNA	0.034±0.003
Suc-Ala-Ala-Pro-Phe-pNA	N.A.
Meo-Suc-Ala-Ala-Pro-Val-pNA	N.A.
	N.A. = No Activity

Table 1 - The specific activity (nmole pNA produced /min/ug protein) of recombinant activated protease D-G-6XHIS, determined for the various substrates analyzed, is shown.

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Compounds that modulate a serine protease of the present invention are identified through screening for the acceleration, or more commonly, the inhibition of the proteolytic activity. Although in the present case chromogenic activity is monitored by an increase in absorbance, fluorogenic assays or other methods such as FRET to measure proteolytic activity as mentioned above, can be employed. Compounds are dissolved in an appropriate solvent, such as DMF, DMSO, methanol, and diluted in water to a range of concentrations usually not exceeding 100 uM and are typically tested, though not limited to, a concentration of 1000-fold the concentration of protease. The compounds are then mixed with the protein stock solution, prior to addition to the reaction mixture. Alternatively, the protein and compound solutions may be added independently to the reaction mixture, with the compound being added either prior to, or immediately after, the addition of the protease D-G protein.

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During the course of these investigations a submission in Genbank was identified (Genbank accession number AF216312) which is similar but distinct from

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the sequence described herein. Although the exact significance of the discrepancy between the protease D-G cDNA and the AF216312 sequence is not fully understood at this time, it may be a result of alternative splicing near the initiator ATG, thereby generating distinct coding sequences and consequently distinct proteins. Below is a

- 5 GAP alignment between the nucleic acid sequences of the protease D-G cDNA (SEQ.ID.NO.:1) described herein on top and in upper case, and the AF216312 sequence indicated below and in lower case.

The Genbank explanatory information is reproduced as follows:

LOCUS AF216312 2079 bp mRNA

- 10 DEFINITION Homo sapiens type II membrane serine protease mRNA, complete cds.

ACCESSION AF216312 VERSION AF216312.1 GI:6911218

SOURCE human.

ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

- 15 REFERENCE 1 (bases 1 to 2079)

AUTHORS Smeekeens,S.S., Lorimer,D.D., Wang,E., Hou,J. and Linnevers,C.

TITLE MT-SP2, a novel type II membrane serine protease expressed in trachea, colon, and small intestine: identification, cloning, and chromosomal localization

JOURNAL Unpublished

- 20 REFERENCE 2 (bases 1 to 2079)

AUTHORS Smeekeens,S.S., Lorimer,D.D., Wang,E., Hou,J. and Linnevers,C.

TITLE Direct Submission

JOURNAL Submitted (14-DEC-1999) Axys Pharmaceuticals, Inc, 180 Kimball Way, South San Francisco, CA 94080, USA

25

SEQ.ID.NO.:1 x AF216312.Seq

- 30 51 CACTCCTGGAATACACAGAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGA 100
 1gagaggcagcagcttggttcagcggacaagga 31
 101 TGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGGGCCTCCTCCAGC 150
 ||||||||||||||||||||||||||||||||||||||||||||||||||||

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32	tgctggg	cgtgaggg	accaagg	cctgcct	ctgcact	cgggc	ctcct	ccagc	81
151	CAGTGTG	TACCAGG	GACTTCT	GACCTG	CTGGCC	AGCCAGG	ACCTGT	GTGTGG	200
82	cagtgtg	taccagg	gacttct	gacctg	ctggcc	agccagg	acctgt	gtgtgg	131
201	GGAGGCC	CTCCTG	CTGCCT	TGGGGT	GACAAT	CTCAGCT	CCAGGCT	ACAGG	250
132	ggaggcc	ctcctg	ctgcct	tgggg	tgacaat	ctcagct	ccaggct	acagg	181
251	GAGACCG	GGAGGAT	CACAGAG	CCAGCAT	GGATCCT	GACAGT	GAT	294
182	gagaccg	ggaggat	cacagag	ccagcat	ggtacag	gatcctg	acagtga	t	231
295	CAACCTC	TGAACAG	CCTCGAT	GTCAAAC	CCCCTG	CGCAAAC	CCCCGTA	TCCC	344
232	caacctc	tgaacag	cctcgat	gtcaaac	cccctg	cgcaaac	ccccgta	tccc	281
345	CATGGAG	ACCTTCA	GAAAG	.GTGGG	GATCCCC	ATCATCA	TAGCACT	ACTG	393
282	catggag	accttc	agaaagt	gtgggg	atcccc	atcatca	tagcact	actg	331
394	AGCCTGG	CGAGTAT	CATCATT	GTGGTT	GTCTCT	CATCAAG	GTGATT	TCTGGA	443
332	agcctgg	cgagtat	catcatt	gtggtt	gtcctca	tcaaggt	gatttct	gga	381
444	TAAATACT	ACTTCC	TCTGCG	GGCAGC	CTCTCC	ACTTCAT	CCCAGG	GAAGC	493
382	taaatac	tacttcc	tctgcg	gggcag	cctctcc	acttcat	cccagga	aagc	431
494	AGCTGTG	TGACGG	AGAGCT	TGGACT	TGCCCT	TGGGGG	GAGGAC	GAGGAC	543
432	agctgtg	tgacgg	agagct	ggactg	tccctt	gggggag	gagacga	ggagcac	481
544	TGTGTCA	AAGAGCT	TCCCCGA	AGGGCCT	TGCAGT	TGGCAGT	CCGCCT	TCTCAA	593
482	tgtgtca	aagagct	tccccga	agggcct	gcagtg	gcagtc	ccgcct	ctcaa	531
594	GGACCGA	TCCACAC	TGCAGG	TGCTGG	ACTCGG	CCACAGG	GAACTGG	TGTCT	643
532	ggaccga	tccacac	tgcagg	tgtggac	tggccac	agggaa	actgggt	tct	581
644	CTGCCTG	TTTCGAC	AACCTT	CACAGA	AGCTCT	CGCTGAG	ACAGCCT	GTAGG	693
582	ctgcctg	tttcgac	aacttc	acagaag	ctctcg	ctgagac	agcctgt	tagg	631
694	CAGATGG	GGCTAC	AGCAGCA	AACCCACT	TTTCA	GAGCTGT	GAGATTG	GGCCC	743
632	cagatgg	ggtacag	cagcaa	accact	tttcag	agctgt	ggagatt	ggccc	681

	744	AGACCAGGATCTGGATGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTC	793
	682	agaccaggatctggtatgttggtgaaatcacagaaaacagccaggagcttc	731
5	794	GCATGCGGA [.] ACTCAAGTGGG [.] CCCTGTCTCTCAGGCTCCCTGGTCTCCCTG	843
	732	gcatg [.] cggaactcaagtggg [.] ccctgtctctcaggctccctgggtctccctg	781
10	844	CACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGG	893
	782	cactgtcttg [.] cctgtgggaagagcctgaagaccccccg [.] tgtggtgggtgg	831
	894	GGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAGTACG	943
15	832	ggaggaggcctctgtggattcttggccttggcaggtcagcatccagtacg	881
	944	ACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTC	993
20	882	acaaacagcacgtctgtggagggagcatcctggacccccactgggtcctc	931
	994	ACGGCAGCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGT	1043
	932	acggcagccca [.] ctgcttcaggaaacataccgatgtgttcaactggaaggt	981
25	1044	GCGGGCAGGCTCAGACAAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCA	1093
	982	gcgggcaggctcagacaaactgggcagcttcccatccctggctgtggcca	1031
	1094	AGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACATC	1143
30	1032	agatcatcatcattgaattcaacccccatgtaccccaaagacaatgacatc	1081
	1144	GCCCTCATGAAGCTGCAGTTCCCACTACTTTCTCAGGCACAGTCAGGCC	1193
35	1082	gccctcatgaagctgcagttccca [.] ctcactttctcaggcacagtcaggcc	1131
	1194	CATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCCTCT	1243
	1132	catctgtctgcccttctttgatgaggagctcactccagccacccccactct	1181
40	1244	GGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGAC	1293
	1182	ggatcattggatggggctttacgaagcagaatggaggggaagatgtctgac	1231
45	1294	ATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGC	1343
	1232	atactgctgcaggcgtcag [.] tccaggtcattgacagcacacgggtgcaatgc	1281
50	1344	AGACGATGCGTACCTGGGGGAAGTCA [.] CCGAGAAGATGATGTGTGCAGGCA	1393

	1282	agacgatgcgtaccagggggaagtacccgagaagatgatgtgtgcaggca	1331
	1394	TCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCCTG	1443
5	1332	tcccggaagggggtgtggacacctgccagggtgacagtgggtgggcccctg	1381
	1444	ATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTA	1493
10	1382	atgtaccaatctgaccagtggcatgtggtgggcatcgttagctggggcta	1431
	1494	TGGCTGCGGGGGCCCGAGCACCCAGGGGTATACACCAAGGTCTCAGCCT	1543
	1432	tggctgcgggggcccagacaccccaggagtatacaccaagggtctcagcct	1481
15	1544	ATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTGTAATGCTGCTGC	1593
	1482	atctcaactggatctacaatgtctggaaggctgagctgtaatgctgctgc	1531
20	1594	CCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCTGGGGA	1643
	1532	ccctttgcagtgctgaggagccgcttccttcctgccctgccacactgggga	1581
	1644	TCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTG	1693
25	1582	tcccccaaagtccagacacagagcaagagtccttccttggtacacccctctg	1631
	1694	CCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGGCCTCAATTCCTATAA	1743
30	1632	cccacagcctcagcatttcttgagcagcaaagggcctcaattcctgtaa	1681
	1744	GAGACCCTCGCAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTC	1793
	1682	gagaccctcgcagcccagaggcgcccagaggaagtcagcagccctagctc	1731
35	1794	GGCCACACTTGGTGCTCCCAGCATCCCAGGGAGAGACACAGCCCACTGAA	1843
	1732	ggccacacttgggtgctcccagcatcccaggagagacacagcccactgaa	1781
40	1844	CAAGGTCTCAGGGGTATTGCTAAGCCAAGAAGGAACTTTCCCACACTACT	1893
	1782	caaggtctcaggggtattgctaagccaagaaggaactttcccacactact	1831
	1894	GAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGGCTGGAGA	1943
45	1832	gaatggaagcaggctgtcttgtaaaagcccagatcactgtgggctggaga	1881
	1944	GGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA	1993
50	1882	ggagaaggaaagggctctgcgccagccctgtccgtcttcacccatccccaa	1931

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1994 GCCTACTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTG.CCTACTG 2042
      |||
1932 gcctactagagcaagaaaccagttgtaatatataaaatgcactgcccactg 1981
      .
5  2043 TTGGTATGACTACCGTTACCTACTGTTGTCAATTGTTATTACAGCTATGGC 2092
      |||
1982 ttggtatgactaccgttacctactgttgtcattgttattacagctatggc 2031
      .
10 2093 CACTATTATTAAAGAGCTGTGTAACATCA..... 2121
      |||
2032 CACTATTATTAAAGAGCTGTGTAACATCAAAAAAAAAAAAAAAAAAAAA 2079

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Below is a GAP alignment between the amino acid sequences of the protease D-G cDNA (SEQ.ID.NO.:2) described herein, on top with the predicted transmembrane domain in lower case, and that encoded by the AF216312 sequence indicated below.

SEQ.ID.NO.:2 x AF216312.Pro

```

20      1 MDPDSDQPLNSLDVKPLRKPRIPMETFRKVgipiiiallslasiiivvv1 50
          | | | | | | | | | | | | | | | | | | | | | | | |
      1 .....MSNPCANPVSPWRPSESVGIIPIIIALLSLASIIIVVVL 38
          . . . . .
25      51 ikVILDKYYFLCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAV 100
          | | | | | | | | | | | | | | | | | | | | | | | |
      39 IKVILDKYYFLCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAV 88
          . . . . .
30      101 AVRLSKDRSTLQVLDSATGNWFSAFCDFNTEALAETACRQMGYSSKPTFR 150
          | | | | | | | | | | | | | | | | | | | | | | | |
      89 AVRLSKDRSTLQVLDSATGNWFSAFCDFNTEALAETACRQMGYSSKPTFR 138
          . . . . .
35      151 AVEIGPDQDLDVVEITENSQELRMRNSSGPGCLSGSLVSLHCLACGKSLKT 200
          | | | | | | | | | | | | | | | | | | | | | | | |
      139 AVEIGPDQDLDVVEITENSQELRMRNSSGPGCLSGSLVSLHCLACGKSLKT 188
          . . . . .
40      201 PRVVGGEASVDSWPWQVSIQYDKQHVCSSILDPHWVLTAAHCFRKHTD 250
          | | | | | | | | | | | | | | | | | | | | | | | |
      189 PRVVGGEASVDSWPWQVSIQYDKQHVCSSILDPHWVLTAAHCFRKHTD 238
          . . . . .
45      251 VFNWKVRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNNDIALMKLQFPLTF 300
          | | | | | | | | | | | | | | | | | | | | | | | |
      239 VFNWKVRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNNDIALMKLQFPLTF 288
          . . . . .
          301 SGTVRPICLPFFDEELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVID 350
          | | | | | | | | | | | | | | | | | | | | | | | |

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351 STRCNADDAYQGEVTEKMMCAGIPEGGVDTTCQGDSSGGLMYQSDQWHVVG 400

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339 STRCNADDAYQGEVTEKMMCAGIPEGGVDTTCQGDSGGPLMYQSDQWHVVG 388

401 IVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 435

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